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(54) Title: P53–REGULATED GENES

(57) Abstract

Many genes are identified as being p53–regulated which were not heretofore known to be p53–regulated. This includes both genes whose expression is induced and genes whose expression is repressed by the expression of wild–type p53. Monitoring expression of these genes is used to provide indications of p53 status in a cell. Such monitoring can also be used to screen for useful anti–cancer therapeutics, as well as for substances which are carcinogenic. Defects in p53 can be bypassed by supplying p53 induced genes to cells. Defects in p53 can also be bypassed by supplying antisense constructs to p53–repressed genes.

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P53-REGULATED GENES

TECHNICAL FIELD OF THE INVENTION

The invention relates to the area of gene regulation, in particular the area of regulation of genes involved in tumorigenesis.

BACKGROUND OF THE INVENTION

P53 is the name of a human tumor suppressor gene and its protein product. About 55 percent of all human cancers from many cell or tissue types suffer mutations in both alleles of the p53 gene. People who have inherited such mutations, will develop cancer over their lifetimes.

The p53 protein is a transcription factor, which regulates the expression of a large number of genes. High levels of an active wild type p53 protein in a cell cause these genes to be transcribed at a high rate. Elucidation of the functions of some of these "p53-regulated or -inducible genes" informs the art of how the p53 protein protects humans from cancers.

There is a need in the art to discover p53-inducible genes and their functions, so that we may have a chance to circumvent the effects of p53 mutations in cancer, by activating the p53-inducible genes and repressing the p53-repressible genes, so as to arrest the cancer's growth. Thus, the elucidation of such p53-regulated genes provides useful and valuable information.

SUMMARY OF THE INVENTION

In one embodiment, a method is provided for diagnosing cancer or for determining p53 status in a sample suspected of being neoplastic. The level of expression of an RNA transcript or its translation product in a first sample of a first tissue is compared to the level of expression of the transcript or translation product in a second sample of a second tissue. The first tissue is suspected of being neoplastic and the second tissue is a normal human tissue. The first and second tissue are of the same tissue type. The transcript is a transcript of a gene selected from the group consisting of gene numbers 1-8, 10, 12, 14-58, 60-68, and 70-100, as shown in Figure 1. The first sample is categorized as neoplastic or as having a mutant p53 when expression is found to be the same or lower in the first sample than in the second sample.

According to another embodiment a method is provided for diagnosing cancer or for determining p53 status in a sample suspected of being neoplastic. The level of expression of an RNA transcript or its translation product in a first sample of a first tissue is compared to the level of expression of the transcript or translation product in a second sample of a second tissue. The first tissue is suspected of being neoplastic and the second tissue is a normal human tissue. The first and second tissue are of the same tissue type. The transcript is a transcript of a gene selected from the group consisting of gene numbers 7-24, and 26-100 as shown in Figure 2. The first sample is categorized as neoplastic or as having a mutant p53 when expression is found to be the same or higher in the first sample than in the second sample.

Another aspect of the invention is a method of diagnosing cancer or determining p53 status in a sample suspected of being neoplastic. The level of expression of at least one RNA transcript or its translation product in a first sample of a first tissue is compared to the level of expression of the transcripts or translation products in a second sample of a second tissue. The first tissue is suspected of being neoplastic and the second tissue is a normal human tissue. The first and second tissue are of the same tissue type. The first group of RNA transcripts consists of transcripts of genes selected from the group of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 as shown in Figure 1. The second group of RNA transcripts consists of

transcripts of genes selected from the group consisting of genes numbered 7-24, and 25-100 as shown in Figure 2. The first sample is categorized as neoplastic or as having a mutant p53 when expression of at least one of the first group of RNA transcripts or translation products is found to be the same or lower in the first sample than in the second sample, and expression of at least one of the second group of transcripts or translation products is found to be the same or higher in the first sample than in the second sample.

According to another aspect of the invention a method is provided for evaluating carcinogenicity of an agent. A test agent is contacted with a human cell. The level of expression of at least one transcript or its translation product is determined in the human cell after contacting with the agent. The transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2. An agent which decreases the level of expression of a gene identified in Figure 1, or an agent which increases the level of expression of a gene identified in Figure 2 is identified as a potential carcinogen.

Another aspect of the invention is directed to a method of treating cancer in a patient. A polynucleotide is administered to cancer cells of a patient. The polynucleotide comprises a coding sequence of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1. The cancer cells of the patient harbor a mutant p53 gene. As a result of the administration, the gene is expressed in cells of the cancer.

Yet another aspect of the invention is directed to a method of treating cancer in a patient. An antisense construct comprising at least 12 nucleotides of a coding sequence of a gene selected from the group consisting of genes numbered 7-24, and 26-100 in Figure 2 is administered to cancer cells of a patient. The coding sequence is in 3' to 5' orientation with respect to a promoter which controls its expression. The cancer cells harbor a mutant p53 gene. As a result of the administration, an antisense RNA is expressed in cells of the cancer.

According to still another aspect of the invention a method is provided of screening for drugs useful in the treatment of cancer. A cell which harbors a p53

mutation is contacted with a test substance. Expression of a transcript or its translation product is monitored. The transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2. A test substance is identified as a potential drug for treating cancer if it increases expression of a gene as shown in Figure 1 or decreases expression of a gene as shown in Figure 2.

Another aspect of the invention is a method of screening for drugs useful in the treatment of cancer. A tumor cell which overexpresses MDM2 is contacted with a test substance. Expression of a transcript or its translation product is monitored. The transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2. A test substance is identified as a potential drug for treating cancer if it increases expression of a gene as shown in Figure 1 or decreases expression of a gene as shown in Figure 2.

Yet another aspect of the invention provides a set of at least two nucleotide probes which hybridize to a set of p53-regulated genes. The genes are selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2.

These and other embodiments of the invention provide the art with methods for diagnosis, treatment and drug discovery for cancers. In addition, it provides a convenient and rapid carcinogenicity test.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a Table showing genes induced by p53. The column headings are as follows. "Eb1" denotes the cell line EB1-α , *i.e.*, a cell line which contains a zinc-inducible p53 gene. "EB" denotes the cell line EB1, a cell line which has a p53 mutant gene that fails to produce or express detectable p53 protein. "PM" denotes the number of perfect match oligonucleotides for a gene which hybridized and "MM" denotes the number of mismatch oligonucleotides for a gene which hybridized. "Ratio" is the ratio of intensity of EB1-α to EB1. "Accession number" refers to a GenBank accession number. "EST?" if checked indicates that the function of the nucleic acid sequence has not been determined. "SAGE?" if checked indicates that analysis using the SAGE

technique also detected this gene as p53-regulated. See http://welchlink.welch.jhu.edu/~molgen-g/P53-SAGE.HTM.

Figure 2 is a Table showing genes repressed by p53. Column headings are the same as in Figure 1.

DETAILED DESCRIPTION

It is a discovery of the present inventors that p53 regulates a whole host of genes, increasing and decreasing expression of their mRNA and protein products. These genes have not previously been identified as p53 regulated. In some cases the biological functions of the genes is unknown. However, the now-established regulation by p53 indicates that the genes are involved in progression and arrest of the cell cycle.

A sampling of 6800 human genes were tested for the effects of p53 expression on their expression. Such a massive screening permits the identification of many genes which were heretofore not known to be p53 regulated.

Genetic status of p53 alleles (mutant or wild-type) has been shown to correlate well with a neoplastic state. Thus diagnosis can be provided based on the status of p53 alleles of cells. The level of expression of an RNA transcript or its translation product can be determined using any techniques known in the art. Specific oligonucleotide probes for the relevant genes can be used in hybridization experiments, as is known in the art. Any hybridization format for determining specific RNA levels can be used, including but not limited to Northern blots, slot blots, dot blots, and hybridization to oligonucleotide arrays. Specificity of hybridization can be assessed by varying degrees of stringency of the hybridization conditions. In addition, comparison of mismatch to perfect match oligonucleotide probes can be used to determine specificity of binding.

To assess specific translation product (protein) expression levels, antibodies specific for the protein can be used readily. Again, any format known in the art for measuring specific protein levels can be used, including sandwich assays, ELISAs, immunoprecipitations, and Western blots. Any of monoclonal antibodies, polyclonal antibodies, single chain antibodies, and antibody fragments may be used in such assays.

Specificity of immunologic reactions can be assessed using competitor antibodies or

proteins, as well as by varying the immunoreaction conditions. Monitoring expression product levels involves determining amounts of a specific expression product. Amounts determined need not be absolute amounts, but may be relative amounts determined under different conditions, for example, in the presence and absence of a test compound.

Probes according to the present invention may be labeled or unlabeled, tethered to another substance or in solution, synthetically made or isolated from nature. Probes can be nucleic acids, either RNA or DNA, which contain naturally occurring nucleotide bases or modified bases. The probes may contain normal nucleotide bonds or peptide bonds. Oligonucleotide probes may be of any length which provides meaningful specificity of hybridization. Thus probes may be as small as 10 nucleotides, and preferably they are between 12 and 30 nucleotides in length. However, oligonucleotide probes may be significantly longer, in the range of 30 to 100 nucleotides, 100 to500 nucleotides or 500 to 2000 nucleotides. Probes may be attached to polymers, either soluble or non-soluble. Probes may be attached or bonded to solid substrates such as filters, sheets, chips, slides, and beads.

High density arrays are particularly useful for monitoring the expression control at the transcriptional, RNA processing and degradation level. The fabrication and application of high density arrays in gene expression monitoring have been disclosed previously in, for example, WO 97/10365, WO 92/10588, U.S. Application Ser. No. 08/772,376 filed December 23, 1996; serial number 08/529,115 filed on September 15, 1995; serial number 08/168,904 filed December 15, 1993; serial number 07/624,114 filed on December 6, 1990, serial number 07/362,901 filed June 7, 1990, all incorporated herein for all purposed by reference. In some embodiments using high density arrays, high density oligonucleotide arrays are synthesized using methods such as the Very Large Scale Immobilized Polymer Synthesis (VLSIPS) disclosed in U.S. Pat. No. 5,445,934 incorporated herein for all purposes by reference. Each oligonucleotide occupies a known location on a substrate. A nucleic acid target sample is hybridized with a high density array of oligonucleotides and then the amount of target nucleic acids hybridized to each probe in the array is quantified. One preferred quantifying method is to use confocal microscope and fluorescent labels.

The GeneChip® system (Affymetrix, Santa Clara, CA) is particularly suitable for quantifying the hybridization; however, it will be apparent to those of skill in the art that any similar systems or other effectively equivalent detection methods can also be used.

Tissue samples which can be tested according to the present invention are any which are derived from a patient, whether human, other domestic animal, or veterinary animal. Vertebrate animals are preferred, such as mice, humans, horses, cows, dogs, and cats, although any organism for which p53 status can be determined may be used. The form of the samples may be any which are routinely used in the art for determining the amounts of specific proteins or mRNA molecules. The samples may be fixed or unfixed, homogenized, lysed, cryopreserved, etc. It is most desirable that matched tissue samples be used as controls. Thus, for example, a suspected colorectal cancer tissue will be compared to a normal colorectal epithelial tissue.

Figures 1 and 2 below show genes which are induced by p53 and repressed by p53, respectively. Genes which are identified with a check in the column headed "SAGE" are those which are believed to be previously identified as p53-regulated. Genes which are not checked are believed to be previously unknown as p53-regulated genes. Genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1, and genes numbered 7-24, and 26-100 in Figure 2, are believed to be such previously unknown p53-regulated genes.

While assaying expression of any single one of the genes identified as p53-regulated may be useful for diagnosis and assays, it may be desirable to use larger sets to confirm the global cellular effects observed. In this regard, it may be desirable to assay for at least 2, 5, 10, 20, 30, 32, 50, 70, or 77 genes of one or both categories of regulation. It may be useful to use both induced and repressed genes to get such a global snapshot of gene regulation.

In a particularly preferred embodiment, oligonucleotide probes for RNA transcripts are attached to solid supports. Such supports are preferably arrays where nucleic acid molecules are attached to the substrate in predetermined positions. In one particular embodiment, the nucleic acid molecules are synthesized on the substrate. In

another embodiment the nucleic acid molecules are applied to the solid support after synthesis or isolation.

Test samples for mRNA are typically harvested from the tissue samples and may be used directly or processed as follows. The sample mRNA is reverse transcribed using reverse transcriptase to form cDNA. A promoter is ligated to the cDNA at its 5', 3', or both ends. (5' and 3' refer to orientation on the coding strand of DNA.) If two promoters are used on one cDNA they can be the same or different. The cDNA is then used as a template to transcribe *in vitro* to form test mRNA. The test RNA can then be used to hybridize to nucleic acid molecules or probes, preferably on a solid support, more preferably on an oligonucleotide array. These processing steps are well known in the art.

The regulated genes discovered here can form the basis of a carcinogenicity test. Test agents are evaluated to see if their effects on human cells mimic the effects of loss of p53. Thus the agents are in essence being evaluated for the ability to induce a p53 mutation, or a mutation in another gene which is in the same regulatory pathway, or a non-genetic effect which mimics p53 loss. Test agents which are found to have at least some of the same constellation of effects as p53 loss on the regulation of the genes identified herein to be p53-regulated, are identified as potential carcinogens. Any single gene identified can be used, as can at least 2, 5, 10, 20, 30, 32, 40, 50, 70, 90, 100, 125, or 145 of the genes identified herein.

The genes identified herein as p53-induced can be delivered therapeutically to cancer cells. Antisense constructs of the genes identified herein as p53-repressed can be delivered therapeutically to cancer cells. The goal of such therapy is to retard the growth rate of the cancer cells. Expression of the sense molecules and their translation products or expression of the antisense mRNA molecules has the effect of inhibiting the growth rate of cancer cells or inducing apoptosis (a radical reduction in the growth rate of a cell). Sense nucleic acid molecules are preferably delivered in constructs wherein a promoter is operatively linked to the coding sequence at the 5'-end and initiates transcription of the coding sequence. Anti-sense constructs contain a promoter operatively linked to the coding sequence at the 3'-end such that upon

initiation of transcription at the promoter an RNA molecule is transcribed which is the complementary strand from the native mRNA molecule of the gene.

Delivery of nucleic acid molecules can be accomplished by many means known in the art. Gene delivery vehicles (GDVs) are available for delivery of polynucleotides to cells, tissue, or to a the mammal for expression. For example, a polynucleotide sequence of the invention can be administered either locally or systemically in a GDV. These constructs can utilize viral or non-viral vector approaches in in vivo or ex vivo modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence in vivo can be either constitutive or regulated. The invention includes gene delivery vehicles capable of expressing the contemplated polynucleotides. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vectors. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, togavirus viral vector. See generally, Jolly, Cancer Gene Therapy 1:51-64 (1994); Kimura, Human Gene Therapy 5:845-852 (1994), Connelly, Human Gene Therapy 6:185-193 (1995), and Kaplitt, Nature Genetics 6:148-153 (1994).

Delivery of the gene therapy constructs of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see Curiel, Hum Gene Ther 3:147-154 (1992) ligand linked DNA, for example, see Wu, J. Biol. Chem. 264:16985-16987 (1989), eucaryotic cell delivery vehicles cells, for example see U.S. Serial No. 08/240,030, filed May 9, 1994, and U.S. Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655, ionizing radiation as described in U.S. Patent No. 5,206,152 and in PCT Patent Publication No. WO 92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, Mol. Cell. Biol. 14:2411-2418 (1994) and in Woffendin, Proc. Natl. Acad. Sci. 91:1581-585 (1994). Particle mediated gene transfer may be

employed, for example see U.S. provisional application No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987), insulin as described in Hucked, Biochem. Pharmacol. 40:253-263 (1990), galactose as described in Plank, Bioconjugate Chem 3:533-539 (1992), lactose or transferrin. Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in PCT Patent Publication No. WO 90/11092 and U.S. Patent No. 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120, PCT Patent Publication Nos. WO 95/13796, WO 94/23697, and WO 91/144445, and EP No. 524,968.

Drugs useful in the treatment of cancer can be screened and identified using the p53-regulated genes disclosed herein. Cells of two types can be contacted with test substances. The cells may not carry a wild-type p53 allele or the cells may overexpress the MDM2 gene product. MDM2 sequesters wild-type p53. Therefore MDM2-overexpressing cells mimic cells which are genetically deficient for p53. Expression of one or more of the p53-regulated genes of the present invention is monitored in the presence of the test substance. A test substance which mimics one or more of the regulatory effects of p53 on the p53-regulated genes is a potential therapeutic agent for treating cancer. Such agents can be subsequently tested in any number of other assays to determine their ultimate usefulness as a drug.

Sets of at least two oligonucleotide probes are provided. Preferably the probes are exclusively perfectly matched probes to the genes. However, mismatch probes having less than 5% mismatched nucleotides can be used. The probes hybridize to the p53-regulated genes disclosed herein in Figures 1 and 2. Particularly useful genes are

those numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1, and those numbered 7-24, and 26-100 in Figure 2. It is preferred that all of the oligonucleotide probes hybridize to p53-regulated genes, although it is permissible to have probes for other genes present which are not p53 regulated. Preferably the probes for other genes comprise less than 50% of the probes, and more preferably comprise less than 25%, 15%, 10%, 5%, 2%, or 1%. The sets of p53 regulated genes may comprise at least five, ten, fifteen, twenty, twenty-five, thirty, fifty, seventy-five, 100, or 140 oligonucleotide probes p53-regulated genes, as disclosed herein. The probes may be attached to a polymer, soluble or insoluble, naturally occurring or synthetic. The probes may be attached to a solid support, in a gel matrix, or in solution. The probes may be individually packaged and contained within a single container, or may be mixed in one or more mixtures. Preferably the probes are arrayed on a solid support.

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention. The following methods were used in the examples reported below.

EXAMPLE

Eb-1 cells were derived from a human colon carcinoma and these cells have a p53 mutant gene that fails to produce or express detectable p53 protein. A p53 wild-type gene was inserted into these cells under the regulation of a metallothionein (MT) promoter. In the presence of zinc, this promoter expresses the p53 gene but in the absence (or low levels) of zinc, little or no p53 mRNA or protein are produced. Thus, p53 mRNA and protein are zinc-inducible and the p53-regulated genes are similarly induced by the addition of zinc. The Eb-1 cells (original cell line) without a p53 inducible wild-type gene are called Eb-1 and Eb-1 cells with the MT-p53 inducible gene are termed Eb-1 (α).

Eb-1 cells and Eb-1 (alpha) cells were grown in culture and either left untreated or exposed to zinc. Four hours and ten hours after the addition of zinc, these cells were harvested for analysis.

The messenger RNA was extracted from these cells and purified. An oligo-dT primer was used to produce a reverse transcriptase copy of the mRNA and then, an oligonucleotide linker was ligated to the end of the cDNA where the linker has a T-7 promoter sequence incorporated into it. All of the cDNAs were cloned into vectors, which were then employed to make mRNA copies *in vitro* using the T-7 RNA polymerase and fluorescent biotinylated nucleotides. The RNA products were hydrolyzed to an average size of 50 nucleotides in length.

The hydrolyzed RNA was hybridized to a chip that contains deoxyoligonucleotide sequence (25 in length) that derive from a database of 6,800 known genes or EST sequences. There is a 20-fold redundancy for each gene or EST sequence and for each perfect sequence match, a mismatched sequence (one base different in the middle of the sequence of 25 nucleotides).

After a short hybridization, that measures the rate (amount) of fluorescent probe hybridized to each set of 20 oligonucleotide sequences, the chips are washed and read by a digital confocal microscope to quantitate the intensity of the fluorescent readout. Gene expression or mRNA concentration is measured by changes in the fluorescent readout for probe pairs. The specificity of the measurements is given by the ratio of hybridization to a perfect sequence matched probe compared with the hybridization to a mismatched probe.

For this experiment a control was run; Eb-1 cells treated or untreated with zinc. Here no p53 cDNA was present so the only variable was the exposure of the cells to zinc. Out of all the genes or sequences tested in these cells (6,800), only six changed their gene expression patterns in response to added zinc and five (1-5) of these six genes are under the control of zinc and cadmium inducible promoters. This experiment serves as an excellent control for the p53 regulation of genes.

For the experiment, Eb-1 (α) cells were treated with zinc or left untreated and at four or ten hours, the cells were harvested. RNA was prepared and processed as described above. The hybridization to the 6,800 different oligonucleotide sequences on the chip (each cDNA had a twenty-fold sequence redundancy covering different sequences in the cDNA) was carried out and the analysis of the data was done by an algorithm. The following criteria were employed to accept a gene as p53-inducible or repressed by p53: (1) the relative intensity of the mRNA hybridization level of an induced gene or a decrease with a repressed gene, was above 160 relative units; this has been shown to be a reproducible level with minimal statistical fluctuations; (2) the fraction of probe pairs (matched hybridized and mismatch not hybridized) had to be 0.85 or greater (17 out of 20 perfect matches); (3) the ratio of induction by p53 or repression by p53, when comparing cellular RNA from Eb-1 zinc-induced cells, was five-fold or greater. Thus, only genes whose mRNA levels increased five-fold or decreased five-fold from a high baseline are reported by this analysis.

Of 6,800 cDNAs detectable on the chip, 70 genes were induced by p53 and 77 were repressed by p53. Once again, there were excellent positive controls in this experiment. The known p53 inducible genes such as p21-WAF-1, IGF-BP-3, MDM-2, GAD-45, as well as some recently reported 53 inducible genes (PIGS) were detected by this chip hybridization. Similarly, a repressed gene, MAP-4 previously reported in the literature was repressed after p53 induction in Eb-1(α) cells as detected in this experiment.

Figure 1 lists the genes which are induced by p53 and Figure 2 lists the genes which are repressed by p53.

CLAIMS

1. A method of diagnosing cancer or determining p53 status in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of an RNA transcript or its translation product in a first sample of a first tissue to the level of expression of the transcript or translation product in a second sample of a second tissue, wherein the first tissue is suspected of being neoplastic and the second tissue is a normal human tissue, wherein the first and second tissue are of the same tissue type, and wherein the transcript is a transcript of a gene selected from the group consisting of gene numbers 1-8, 10, 12, 14-58, 60-68, and 70-100, as shown in Figure 1;

categorizing the first sample as neoplastic or as having a mutant p53 when expression is found to be the same or lower in the first sample than in the second sample.

2. A method of diagnosing cancer or determining p53 status in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of an RNA transcript or its translation product in a first sample of a first tissue to the level of expression of the transcript or translation product in a second sample of a second tissue, wherein the first tissue is suspected of being neoplastic and the second tissue is a normal human tissue, wherein the first and second tissue are of the same tissue type, and wherein the transcript is a transcript of a gene selected from the group consisting of gene numbers 7-24, and 26-100 as shown in Figure 2;

categorizing the first sample as neoplastic or as having a mutant p53 when expression is found to be the same or higher in the first sample than in the second sample.

3. The method of claim 1 wherein a comparison of at least two of the transcripts or translation products is performed.

4. The method of claim 2 wherein a comparison of at least two of the transcripts or translation products is performed.

5. The method of claim 1 wherein a comparison of at least five of the transcripts or translation products is performed.

6. The method of claim 2 wherein a comparison of at least five of the transcripts or translation products is performed.

7. The method of claim 1 wherein a comparison of at least ten of the transcripts or translation products is performed.

8. The method of claim 2 wherein a comparison of at least ten of the transcripts or translation products is performed.

9. The method of claim 1 wherein a comparison of at least twenty of the transcripts or translation products is performed.

10. The method of claim 2 wherein a comparison of at least twenty of the transcripts or translation products is performed.

11. The method of claim 1 wherein a comparison of at least 32 of the transcripts or translation products is performed.

12. The method of claim 2 wherein a comparison of at least 32 of the transcripts or translation products is performed.

13. The method of claim 1 wherein a comparison of at least fifty of the transcripts or translation products is performed.

14. The method of claim 2 wherein a comparison of at least fifty of the transcripts or translation products is performed.

15. The method of claim 1 wherein a comparison of 70 of the transcripts or translation products is performed.

16. The method of claim 2 wherein a comparison of 77 of the transcripts or translation products is performed.

17. A method of diagnosing cancer or determining p53 status in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one RNA transcript or its translation product in a first sample of a first tissue to the level of expression of the transcripts or translation products in a second sample of a second tissue, wherein the first tissue is suspected of being neoplastic and the second tissue is a normal human tissue, wherein the first and second tissue are of the same tissue type, and wherein the

first group of RNA transcripts consists of transcripts of genes selected from the group of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 as shown in Figure 1 and wherein the second group of RNA transcripts consists of transcripts of genes selected from the group consisting of genes numbered 7-24, and 25-100 as shown in Figure 2;

categorizing the first sample as neoplastic or as having a mutant p53 when expression of at least one of the first group of RNA transcripts or translation products is found to be the same or lower in the first sample than in the second sample, and expression of at least one of the second group of transcripts or translation products is found to be the same or higher in the first sample than in the second sample.

18. The method of claim 17 wherein a comparison of at least two of the transcripts or translation products in each group of transcripts or translation products is performed.

19. The method of claim 17 wherein a comparison of at least five of the transcripts or translation products in each group of transcripts or translation products is performed.

20. The method of claim 17 wherein a comparison of at least ten of the transcripts or translation products in each group of transcripts or translation products is performed.

21. The method of claim 17 wherein a comparison of at least twenty of the transcripts or translation products in each group of transcripts or translation products is performed.

22. The method of claim 17 wherein a comparison of at least thirty of the transcripts or translation products in each group of transcripts or translation products is performed.

23. The method of claim 17 wherein a comparison of at least fifty of the transcripts or translation products in each group of transcripts or translation products is performed.

24. The method of claim 17 wherein a comparison of at least seventy of the transcripts or translation products in each group of transcripts or translation products is performed.

25. The method of claim 1 wherein the level of expression of the RNA transcripts is determined using an array of nucleic acid molecules attached to a substrate in predetermined positions.

26. The method of claim 2 wherein the level of expression of the RNA transcripts is determined using an array of nucleic acid molecules attached to a substrate in predetermined positions.

27. The method of claim 17 wherein the level of expression of the RNA transcripts is determined using arrays of nucleic acid molecules attached to a substrate in predetermined positions.

28. The method of claim 1 wherein the level of expression of the RNA transcript is determined by a method comprising the steps of:

harvesting sample mRNA from the samples;

reverse transcribing the sample mRNA to form DNA;

ligating a promoter to the DNA;

transcribing *in vitro* using the DNA as a template to form test mRNA;

hybridizing the test RNA to an array of nucleic acid molecules.

29. The method of claim 2 wherein the level of expression of the RNA transcript is determined by a method comprising the steps of:

harvesting sample mRNA from the samples;

reverse transcribing the sample mRNA to form DNA;

ligating a promoter to the DNA;

transcribing *in vitro* using the DNA as a template to form test mRNA;

hybridizing the test RNA to an array of nucleic acid molecules.

30. The method of claim 17 wherein the level of expression of the RNA transcript is determined by a method comprising the steps of:

harvesting sample mRNA from the samples;

reverse transcribing the sample mRNA to form DNA;

ligating a promoter to the DNA;

transcribing *in vitro* using the DNA as a template to form test mRNA;

hybridizing the test RNA to an array of nucleic acid molecules.

31. A method for evaluating carcinogenicity of an agent, comprising the steps of:

contacting a test agent with a human cell;

determining the level of expression of at least one transcript or its translation product in the human cell after contacting with the agent; wherein the transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2, wherein an agent which decreases the level of expression of a gene identified in Figure 1, or an agent which increases the level of expression of a gene identified in Figure 2 is a potential carcinogen.

32. The method of claim 31wherein determining the level of expression of at least two of the transcripts or translation products is performed.

33. The method of claim 31wherein determining the level of expression of at least five of the transcripts or translation products is performed.

34. The method of claim 31wherein determining the level of expression of at least ten of the transcripts or translation products is performed.

35. The method of claim 31wherein determining the level of expression of at least twenty of the transcripts or translation products is performed.

36. The method of claim 31wherein determining the level of expression of at least fifty of the transcripts or translation products is performed.

37. The method of claim 31wherein determining the level of expression of 70 of the transcripts or translation products is performed.

38. The method of claim 31wherein determining the level of expression of 90 of the transcripts or translation products is performed.

39. The method of claim 31wherein determining the level of expression of 100 of the transcripts or translation products is performed.

40. The method of claim 31wherein determining the level of expression of 125 of the transcripts or translation products is performed.

41. The method of claim 31wherein determining the level of expression of 145 of the transcripts or translation products is performed.

42. A method of treating cancer in a patient, comprising the step of:

administering to cancer cells of a patient a polynucleotide comprising a coding sequence of a gene selected from the group consisting of genes numbered 1-8, 10, 12,

14-58, 60-68, and 70-100 in Figure 1, wherein the cancer cells of the patient harbor a mutant p53 gene, whereby the gene is expressed in cells of the cancer.

43. A method of treating cancer in a patient, comprising the step of:

administering to cancer cells of a patient an antisense construct comprising at least 12 nucleotides of a coding sequence of a gene selected from the group consisting of genes numbered 7-24, and 26-100 in Figure 2, wherein the coding sequence is in 3' to 5' orientation with respect to a promoter which controls its expression, wherein the cancer harbors a mutant p53 gene; whereby an antisense RNA is expresed in cells of the cancer.

44. A method of screening for drugs useful in the treatment of cancer, comprising:

contacting a cell which harbors a p53 mutation with a test substance;

monitoring expression of a transcript or its translation product, wherein the transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2, wherein a test substance is identified as a potiential drug for treating cancer if it increases expression of a gene as shown in Figure 1or decreases expression of a gene as shown in Figure 2.

45. A method of screening for drugs useful in the treatment of cancer, comprising:

contacting a tumor cell which overexpresses MDM2 with a test substance;

monitoring expression of a transcript or its translation product, wherein the transcript is of a gene selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2, wherein a test substance is identified as a potiential drug for treating cancer if it increases expression of a gene as shown in Figure 1or decreases expression of a gene as shown in Figure 2.

46. A set of at least two oligonucleotide probes which hybridize to a set of p53-regulated genes, wherein the genes are selected from the group consisting of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2.

47. The set of claim 46 which comprises five oligonucleotide probes.

48. The set of claim 46 which comprises ten oligonucleotide probes.

49. The set of claim 46 which comprises fifteen oligonucleotide probes.

50. The set of claim 46 which comprises twenty oligonucleotide probes.

51. The set of claim 46 which comprises twenty-five oligonucleotide probes.

52. The set of claim 46 which comprises thirty oligonucleotide probes.

53. The set of claim 46 which comprises fifty oligonucleotide probes.

54. The set of claim 46 which comprises seventy-five oligonucleotide probes.

55. The set of claim 46 which comprises 100 oligonucleotide probes.

56. The set of claim 46 which comprises 140 oligonucleotide probes.

57. The set of claim 46 wherein the probes are attached to a polymer.

58. The set of claim 46 wherein the probes are attached to a solid support.

59. The set of claim 46 which comprises probes which hybridize to each of genes numbered 1-8, 10, 12, 14-58, 60-68, and 70-100 in Figure 1 and genes numbered 7-24, and 26-100 in Figure 2.

60. The set of claim 46 wherein the probes are in a gel matrix.

61. The set of claim 46 wherein the probes are in solution.

62. The set of claim 46 wherein the probes are individually packaged in a single container.

63. The set of claim 46 wherein the probes are arrayed on a solid support.

64. The method of claim 1 wherein an immunoassay is performed to determine the level of expression.

65. The method of claim 2 wherein an immunoassay is performed to determine the level of expression.

66. The method of claim 17 wherein an immunoassay is performed to determine the level of expression.

FIG. 1A

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Induced Ratio	EST #	Accession #	EST?	SAGE?
1	1450	-36.7	0.85	0.35		Hsa.140	M87789 gene 1	☑	☐
2	1450	107	1	0.7	14	Hsa.1534	J00231 gene 1	☐	☐
3	1220	-30.9	0.95	0.45		Hsa.20518	R85690 3' UTR 2a	☑	☐
4	1070	86.4	1	0.7	12	Hsa.8219	R46753 3' UTR 2a	☑	☐
5	1010	155	0.95	0.7	6	Hsa.2820	Z31695 gene 1	☐	☐
6	1010	53.4	1	0.67	19	Hsa.41163	U06088 gene 1	☐	☐
7	864	46.4	1	0.81	19	Hsa.2836	R71870 3' UTR 1	☑	☐
8	862	148	0.9	0.9	6	Hsa.2551	X57348 gene 1	☐	☐
9	788	137	0.85	0.7	6	Hsa.41123	J00277 gene 1	☐	☑
10	714	139	1	0.95	5	Hsa.13765	X55740 gene 1	☐	☐
11	695	-4.82	1	0.62		Hsa.224	U03106 gene 1	☐	☑
12	645	98.6	0.9	0.8	7	Hsa.8966	X80200 gene 1	☐	☐
13	599	-3.31	1	0.42		Hsa.224	U03106 gene 1	☐	☑
14	582	45.8	0.85	0.55	13	Hsa.1556	L13738 gene 1	☐	☐
15	572	10.5	0.85	0.6	54	Hsa.9103	T67406 3' UTR 2a	☑	☐
16	569	46.4	0.95	0.52	12	Hsa.3081	H20434 3' UTR 1	☐	☐
17	538	-99.1	0.93	0.47		Hsa.936	Z20656 gene 1	☐	☐
18	515	25.5	0.95	0.5	20	Hsa.866	M21389 gene 1	☑	☐
19	480	48.1	0.95	0.85	10	Hsa.36025	H28050 3' UTR 2a	☑	☐
20	473	31.7	0.9	0.7	15	Hsa.1464	M35878 gene 1	☐	☐
21	463	6.03	0.9	0.4		Hsa.1971	T51913 3' UTR 1	☑	☐
22	445	-9.41	0.94	0.47		Hsa.3011	X63380 gene 1	☐	☐

TO FIG. IB

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FIG. 1B

TO FIG. 1A

23	437	-6.03	0.9	0.5		Hsa.21756	R94967 3' UTR 2a	☑	☐
24	385	32.8	0.95	0.55	12	Hsa.1069	T41265 3' UTR 1	☐	☐
25	383	61.2	0.8	0.65	6	Hsa.32222	R69448 3' UTR 2a	☑	☐
26	383	21.9	1	0.75	17	Hsa.2611	R59199 3' UTR 1	☑	☐
27	376	10.5	0.94	0.59	36	Hsa.620	M27138 gene 1	☐	☐
28	364	61.1	0.9	0.6	6	Hsa.401	X82166 gene 1	☐	☐
29	353	-34.4	0.85	0.5		Hsa.936	Z20656 gene 1	☐	☐
30	341	-42.5	0.95	0.48		Hsa.3064	X05615 gene 1	☐	☐
31	331	21.1	0.81	0.52	16	Hsa.243	U01147 gene 1	☐	☐
32	329	54	1	0.94	6	Hsa.1432	M64347 gene 1	☐	☐
33	313	55.6	0.95	0.8	6	Hsa.32445	R71505 3' UTR 2a	☑	☐
34	293	13.3	0.9	0.55	22	Hsa.3348	X15880 gene 1	☐	☐
35	291	18.7	0.9	0.7	16	Hsa.2000	L16242 gene 1	☐	☐
36	288	-18.3	0.9	0.45		Hsa.8468	H19201 3' UTR 2a	☑	☐
37	287	17	0.9	0.62	17	Hsa.169	U02388 gene 1	☐	☐
38	276	40.7	1	0.78	7	Hsa.41094	L18920 gene 1	☐	☐
39	275	37.4	0.9	0.9	7	Hsa.2054	X70340 gene 1	☐	☐
40	269	38.1	0.95	0.8	7	Hsa.21901	R49565 3' UTR 1	☐	☐
41	252	-30.5	0.76	0.48		Hsa.1876	X54156 gene 1	☐	☐
42	250	48.2	0.9	0.55	5	Hsa.2827	Z11502 gene 1	☐	☐
43	247	25.5	1	0.69	10	Hsa.2835	X07696 gene 1	☑	☐

FIG. 1C

Gene Description	Induced
IG GAMMA-1 CHAIN C REGION (HUMAN);.	
Human Ig gamma3 heavy chain disease OMM protein mRNA.	
274912 MYELIN TRANSCRIPTION FACTOR 1 (Homo sapiens)	
152524 CYCLIN-DEPENDENT KINASE INHIBITOR 1 (Homo sapiens)	
H.sapiens mRNA for 43 kDa inositol polyphosphate 5-phosphatase.	
Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.	
155730 KERATIN, TYPE I CYTOSKELETAL 17 (HUMAN);.	
H.sapiens mRNA (clone 9112), kinase related protein.	
c-Ha-ras1 proto-oncogene, complete coding sequence, Human (genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3,4, 6]).	
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).	
Human wild-type p53 activated fragment-1 (WAF1) mRNA, complete cds.	
H.sapiens MLN62 mRNA.	
Human wild-type p53 activated fragment-1 (WAF1) mRNA, complete cds.	
Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	
81780 COMPLEMENT C4 PRECURSOR (Homo sapiens)	
172486 clone, mRNA for tuberin, or TSC2 gene.	
Homo sapiens of cardiac alpha-myosin heavy chain gene.	
KERATIN, TYPE II CYTOSKELETAL 5 (HUMAN);contains MSR1 repetitive element ;.	
182000 FK506-BINDING PROTEIN PRECURSOR (Mus musculus)	
Human insulin-like growth factor-binding protein-3 gene, complete cds, clone HL1006d.	
72466 ALPHA CRYSTALLIN B CHAIN (HUMAN).	
Homo sapiens mRNA for serum response factor-related protein, RSRFR2.	

TO FIG. ID

FIG. 1D

TO FIG. IC

198656 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (Homo sapiens)
62461 SMALL NUCLEAR RIBONUCLEORPROTEIN Particle N (SNRPN), contains MSR1 repetitive element,.
155335 INTEGRIN ALPHA-3 (Homo sapiens)
41792 TUBULIN BETA-2 CHAIN (HUMAN);.
Human estradiol 17 beta-dehydrogenase gene, complete cds.
H.sapiens mRNA for cystathionine-beta-synthase.
Homo sapiens of cardiac alpha-myosin heavy chain gene.
Human mRNA for thyroglobulin.
Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds.
Human novel growth factor receptor mRNA, 3' cds.
142899 DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (Plasmodium falciparum)
Human mRNA for collagen VI alpha-1 C-terminal globular domain.
Homo sapiens sodium channel type I, beta subunit (SCN1B) mRNA, complete cds.
50887 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDSA (Mus musculus)
Human cytochrome P450 4F2 (CYP4F2) mRNA, complete cds.
Human MAGE-2 gene exons 1-4, complete cds.
H.sapiens mRNA for transforming growth factor alpha.
38251 H.sapiens HSJ1 mRNA.
p53
H.sapiens mRNA for intestine-specific annexin.
KERATIN, TYPE I CYTOSKELETAL 15 (HUMAN);contains MER20 repetitive element ;.

FIG. 1E

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Induced Ratio	EST #	Accession #	EST?	SAGE?
44	245	26.2	0.8	0.55	9	Hsa.35663	H24346 3' UTR 2a	☑	☐
45	245	19.6	0.9	0.5	12	Hsa.3189	U17280 gene 1	☐	☐
46	239	47.6	0.9	1	5	Hsa.1915	L06419 gene 1	☑	☐
47	232	32.8	0.85	0.5	7	Hsa.33725	H04238 3' UTR 2a	☑	☐
48	225	-53.5	0.85	0.4		Hsa.693	L31409 gene 1	☐	☐
49	222	18.7	0.94	0.71	12	Hsa.2835	X07696 gene 1	☑	☐
50	218	-0.125	1	0.38		Hsa.2072	Y00406 gene 1	☐	☐
51	217	-28.8	0.9	0.43		Hsa.1159	R85613 3' UTR 1	☑	☐
52	215	-13.5	0.82	0.71		Hsa.19576	T98002 3' UTR 2a	☑	☐
53	212	-22.4	0.81	0.38		Hsa.407	M95167 gene 1	☐	☐
54	210	39.5	1	0.8	5	Hsa.31500	R62945 3' UTR 2a	☑	☐
55	204	-2.31	0.86	0.43		Hsa.2625	Z18951 gene 1	☐	☐
56	199	8.4	0.85	0.4		Hsa.3344	M74509 gene 1	☐	☐
57	199	32	0.85	0.5	6	Hsa.3893	R42765 3' UTR 2a	☑	☐
58	198	15.2	0.86	0.62	13	Hsa.2112	L07597 gene 1	☐	☐
59	194	11.6	0.92	0.33	17	Hsa.1382	U06643 gene 1	☐	☑
60	192	18.1	0.9	0.7	11	Hsa.2208	M67454 gene 1	☐	☐
61	190	-12.6	0.9	0.45		Hsa.2729	V00511 gene 1	☐	☐
62	189	-6.86	0.91	0.45		Hsa.2947	X54936 gene 1	☐	☐
63	183	-20.9	1	0.5		Hsa.2947	X54936 gene 1	☐	☐
64	182	20.9	0.94	0.76	9	Hsa.1870	M79463 gene 1	☐	☐

TO FIG. IF

FIG. 1F

TO FIG. 1E

65	180	27.7	0.9	0.6	6	Hsa.36694	D25217 gene 1	☐	☐
66	178	-77.8	0.89	0.22		Hsa.772	M38451 gene 1	☐	☐
67	178	-39.7	0.9	0.38		Hsa.2402	L36069 gene 1	☐	☐
68	176	-249	0.85	0.35		Hsa.967	M33388 gene 1	☐	☐
69	175	-4.32	0.95	0.45		Hsa.837	M10755 gene 1	☑	☑
70	165	20.7	1	0.76	8	Hsa.37262	R84974 3' UTR 2a	☑	☐
71	165	30.1	0.95	0.7	5	Hsa.27577	R48578 3' UTR 2a	☑	☐
72	165	31.1	0.9	0.65	5	Hsa.25777	R62459 3' UTR 2a	☑	☐
73	163	25.6	0.8	0.7	6	Hsa.35954	H26960 3' UTR 2a	☑	☐
74	161	-10.4	0.9	0.5		Hsa.1842	M94547 gene 1	☑	☐
75	157	8.9	0.95	0.6		Hsa.218	T64470 3' UTR 1	☑	☐
76	154	26.3	0.76	0.62	6	Hsa.19553	T97948 3' UTR 2a	☑	☐
77	147	6.01	0.95	0.65		Hsa.1387	U14631 gene 1	☐	☐
78	141	15.1	0.85	0.7	9	Hsa.2823	L05072 gene 1	☐	☐
79	141	20	0.86	0.79	7	Hsa.2208	M67454 gene 1	☐	☐
80	141	3.08	0.95	0.65		Hsa.955	M32011 gene 1	☑	☐
81	140	10.1	1	0.48	14	Hsa.3279	U28249 gene 1	☐	☐
82	136	7.45	0.95	0.71		Hsa.9537	U28369 gene 1	☐	☐
83	132	6.17	0.81	0.48		Hsa.1846	M96980 gene 1	☑	☐
84	119	-8.34	0.88	0.76		Hsa.36766	H40980 3' UTR 2a	☑	☐
85	118	-6.81	0.8	0.6		Hsa.1221	T60155 3' UTR 1	☑	☐
86	117	12.3	0.9	0.6	10	Hsa.2826	X07876 gene 1	☐	☐

FIG. 1G

Gene Description	Induced
52065 GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 (Homo sapiens)	
Human steroidogenic acute regulatory protein (StAR) mRNA, complete cds.	
LYSYL HYDROXYLASE (PLOD), (HUMAN)	
151767 FASL RECEPTOR PRECURSOR (Homo sapiens)	
Homo sapiens creatine transporter mRNA, complete cds.	
KERATIN, TYPE I CYTOSKELETAL 15 (HUMAN);contains MER20 repetitive element ;.	
Human mRNA for thyroperoxidase.	
275040 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (HUMAN);.	
121731 CYTOCHROME P450 IVB1 (Rattus norvegicus)	
Homo sapiens dopamine transporter (SLC6A3) mRNA, complete cds.	
139080 COMPLEMENT DECAY-ACCELERATING FACTOR 1 PRECURSOR (Homo sapiens)	
H sapiens mRNA for caveolin.	
Human endogenous retrovirus type C oncovirus sequence.	
31481 TYROSINE-PROTEIN KINASE HCK (Homo sapiens)	
Homo sapiens ribosomal protein S6 kinase 2 (RPS6KA2) mRNA, complete cds.	
Human keratinocyte lectin 14 (HKL-14) mRNA, complete cds.	
Human Fas antigen (fas) mRNA, complete cds.	
Human mRNA encoding pregastrin (a regulatory hormone of gastric acid secretin and growth of the gastrointestinal mucosa).	
H.sapiens mRNA for placenta growth factor (PIGF).	
H.sapiens mRNA for placenta growth factor (PIGF).	
Human PML-2 mRNA, complete CDS.	

TO FIG. 1H

FIG. 1H

TO FIG. IG

Human mRNA (KIAA0027) for ORF, partial cds.
Human placenta-specific growth hormone mRNA, complete cds.
Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds.
Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
INTERFERON-INDUCED 17 KD/ 15 KD PROTEIN (HUMAN)
180447 FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (Homo sapiens)
153585 EBNA-2 NUCLEAR PROTEIN (Epstein-barr virus)
36678 TROPONIN C, ISOFORM 2 (Balanus nubilis)
182125 HDL-BINDING PROTEIN
HUMMLC2At; Homo sapiens: 593 base-pairs
80486 LIVER CARBOXYLESTERASE PRECURSOR (HUMAN);.
121916 NEUTRAL CALPONIN, SMOOTH MUSCLE (Sus scrofa)
Human 11 beta-hydroxysteroid dehydrogenase type II mRNA, complete cds.
Homo sapiens interferon regulatory factor 1 gene, complete cds.
Human Fas antigen (fas) mRNA, complete cds.
NEUTROPHIL OXIDASE FACTOR (p67 PHOX) (HUMAN)
Human 11kd protein mRNA, complete cds.
Human semaphorin V mRNA, complete cds.
MYELIN TRANSCRIPTION FACTOR 1 (HUMAN);.
175991 NEURONAL CALCIUM SENSOR 1 (Rattus norvegicus)
81422 HUMAN SMOOTH MUSCLE ALPHA-ACTIN (AORTIC TYPE)
Human mRNA for irp protein (int-1 related protein).

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FIG. 1I

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Induced Ratio	EST #	Accession #	EST?	SAGE?
87	117	1.9	0.92	0.5		Hsa.2208	M67454 gene 1	☐	☐
88	107	-21.3	0.8	0.45		Hsa.1881	M14083 gene 1	☐	☐
89	107	-0.81	0.8	0.55		Hsa.22529	R37128 3' UTR 2a	☑	☐
90	106	0.0333	1	0.5		Hsa.10171	R70008 3' UTR 2a	☑	☐
91	105	8.36	0.85	0.7		Hsa.2325	U14747 gene 1	☐	☐
92	105	-6.04	0.9	0.38		Hsa.2980	X77737 gene 1	☐	☐
93	104	14.7	0.9	0.7	7	Hsa.2131	L25541 gene 1	☐	☐
94	103	-168	0.87	0.47		Hsa.967	M33388 gene 1	☐	☐
95	89	-5.05	0.9	0.6		Hsa.1497	M75126	☐	☐
96	85.9	6.79	0.81	0.57		Hsa.2013	Z12020 gene 1	☐	☐
97	84.6	11.9	0.9	0.65	7	Hsa.101	D12620 gene 1	☐	☐
98	82.8	2.73	0.95	0.5		Hsa.1984	J05200 gene 1	☑	☐
99	81.5	11.1	0.85	0.65	7	Hsa.27854	R51856 3' UTR 2a	☑	☐
100	79.9	-0.934	0.9	0.45		Hsa.20474	R01072 3' UTR 2a	☑	☐

FIG. 1J

Gene Description:	Induced
Human Fas antigen (fas) mRNA, complete cds.	
Human beta-migrating plasminogen activator inhibitor I mRNA, 3' end.	
26063 COMPLEMENT C4 PRECURSOR (Homo sapiens)	
142450 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (Rattus norvegicus)	
Human visinin-like peptide 1 homolog mRNA, complete cds.	
H.sapiens mRNA for red cell anion exchanger (EPB3, AE1, Band 3) 3' non-coding region.	
Human laminin S B3 chain (LAMB3) mRNA, complete cds.	
Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.	
Human hexokinase 1 (HK1) mRNA, complete cds.	
Human mRNA for the MDM2 gene.	
Human mRNA for cytochrome P-450LTBV.	
RYANODINE RECEPTOR, SKELETAL MUSCLE (HUMAN);.	
39052 POTASSIUM CHANNEL PROTEIN EAG (Drosophila melanogaster)	
124416 SERINE THREONINE-PROTEIN KINASE COT-1 (Neurospora crassa)	

PCT/US99/06656

FIG. 2A

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Repressed Ratio	EST #	Accession #	EST?	SAGE?
1	400	2750	0.95	1	6.9	Hsa.1137	T57686 3' UTR 1	☑	☑
2	323	2600	0.75	1	8.04	Hsa.10770	T76971 3' UTR 1	☐	☑
3	411	2300	1	1	5.59	Hsa.1047	R84411 3' UTR 1	☑	☑
4	261	2010	0.75	0.85	7.7	Hsa.2715	H77597 3' UTR 1	☐	☑
5	156	1970	0.95	1	12.7	Hsa.14842	T90759 3' UTR 2a	☑	☑
6	303	1770	1	1	5.83	Hsa.18397	R81812 3' UTR 2a	☑	☑
7	209	1580	0.85	1	7.57	Hsa.1311	R91912 3' UTR 1	☑	☐
8	311	1570	0.95	1	5.05	Hsa.1205	R08183 3' UTR 1	☑	☐
9	245	1460	0.95	1	5.95	Hsa.2806	X77956 gene 1	☐	☐
10	253	1450	0.75	0.95	5.75	Hsa.11673	H23544 3' UTR 2a	☑	☐
11	246	1410	0.9	1	5.73	Hsa.1190	T74556 3' UTR 1	☑	☐
12	62	1350	0.9	1	21.8	Hsa.1505	M12623 gene 1	☐	☐
13	201	1170	0.8	1	5.84	Hsa.1896	J04173 gene 1	☑	☐
14	178	1110	0.9	1	6.23	Hsa.122	D14696 gene 1	☐	☐
15	176	1100	0.9	1	6.24	Hsa.17649	T87527 3' UTR 2a	☑	☐
16	183	1060	0.9	1	5.8	Hsa.1013	T61661 3' UTR 1	☑	☐
17	102	1030	0.7	0.95	10.1	Hsa.1401	R02151 3' UTR 1	☑	☐
18	120	1020	0.9	1	8.48	Hsa.18401	R23889 3' UTR 2a	☑	☐
19	96.4	999	0.85	1	10.4	Hsa.1676	H73758 3' UTR 1	☑	☐
20	146	876	0.85	1	5.99	Hsa.1617	D43950 gene 1	☐	☐
21	3.17	867	0.5	0.95		Hsa.115	D14657 gene 1	☐	☐

TO FIG. 2B

FIG. 2B

TO FIG. 2A

22	154	804	0.7	0.95	5.22	Hsa.12893	H49652 3' UTR 2a	☑	☐
23	105	632	0.95	1	6.04	Hsa.1043	M29065 gene 1	☐	☐
24	64.5	602	0.75	0.8	9.34	Hsa.448	H09351 3' UTR 1	☑	☐
25	61.4	556	0.6	1	9.05	Hsa.6472	T56604 3' UTR 2a	☑	☑
26	48.7	525	0.7	1	10.8	Hsa.1778	J04977 gene 1	☐	☐
27	26.4	495	0.65	0.9	18.8	Hsa.2965	Y00705 gene 1	☐	☐
28	37.3	491	0.75	0.95	13.2	Hsa.1422	M13450 gene 1	☐	☐
29	93.9	487	0.85	1	5.19	Hsa.1046	H29485 3' UTR 1	☑	☐
30	93.6	486	0.85	0.95	5.2	Hsa.3037	X74104 gene 1	☐	☐
31	57.1	468	0.7	0.85	8.19	Hsa.10011	R06239 3' UTR 2a	☑	☐
32	84.5	456	0.85	0.95	5.4	Hsa.347	D16111 gene 1	☐	☐
33	66	444	0.71	1	6.73	Hsa.9937	T94834 3' UTR 2a	☑	☐
34	54.8	423	0.76	0.86	7.72	Hsa.3253	U14603 gene 1	☐	☐
35	26.7	414	0.8	1	15.5	Hsa.1786	L25941 gene 1	☐	☐
36	48.4	403	0.8	1	8.31	Hsa.14831	H29320 3' UTR 2a	☑	☐
37	45.8	400	0.8	0.85	8.74	Hsa.1606	X64330 gene 1	☐	☐
38	62	395	0.9	0.95	6.37	Hsa.116	D14658 gene 1	☐	☐
39	62.4	391	0.86	0.86	6.27	Hsa.3318	H65116 3' UTR 1	☑	☐
40	4.31	364	0.55	0.95		Hsa.13508	R37660 3' UTR 2a	☑	☐
41	66.9	351	0.8	1	5.25	Hsa.2959	X74330 gene 1	☐	☐
42	12.1	327	0.52	0.9	27	Hsa.1343	M13665 gene 1	☐	☐
43	44.4	313	0.59	0.88	7.05	Hsa.2459	U10116 gene 1	☐	☐

FIG. 2C

Repressed Gene Description
79398 TUBULIN ALPHA-1 CHAIN (HUMAN).
113739 H.sapiens mRNA for metallothionein (HUMAN);.
194660 SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEINS B AND B' (HUMAN);.
214162 H.sapiens mRNA for metallothionein (HUMAN);.
111435 TUBULIN ALPHA-1 CHAIN (Gallus gallus)
HUMAN mRNA FOR ADENOCARCINOMA-ASSOCIATED ANTIGEN (KSA), or GA733-2
196105 PLACENTAL CALCIUM-BINDING PROTEIN (HUMAN);.
127228 HEAT SHOCK PROTEIN, CHAPERONIN 10, or GroES; MITOCHONDRIAL ;.
H.sapiens Id1 mRNA.
51894 GTP-BINDING NUCLEAR PROTEIN RAN (Homo sapiens)
84680 ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);.
Human non-histone chromosomal protein HMG-17 mRNA, complete cds.
PHOSPHOGLYCERATE MUTASE, BRAIN FORM (HUMAN).
Human mRNA (KIAA0108) for ORF (complete cds) and HepG2 mRNA identical sequence.
115413 HEAT SHOCK PROTEIN HSP 84 (Mus musculus).
78161 PROFILIN I (HUMAN)
124693 RAT mRNA for PROTEASOME SUBUNIT RC10-II, or HUMAN PROTEASOME SUBUNIT HSC10-II.
131036 TRANSFERRIN RECEPTOR PROTEIN (Homo sapiens)
214923 PSORIASIS-ASSOCIATED FATTY ACID BINDING PROTEIN HOMOLOG (HUMAN);.
Human mRNA (KIAA0098) for ORF (human counterpart of mouse chaperonin containing TCP-1 gene), partial cds.
Human mRNA for ORF(KIAA0101), comlpete cds.

TO FIG. 2D

FIG. 2D

TO FIG. 2C

274422 ATPASE INHIBITOR, MITOCHONDRIAL (BOVIN).
Human hnRNP A2 protein mRNA.
46019 MCM3 HOMOLOG (HUMAN);.
73143 TUBULIN BETA-1 CHAIN (Haliotis discus)
Human Ku autoimmune antigen gene, complete cds.
Homo sapiens pstI mRNA for pancreatic secretory inhibitor (expressed in neoplastic tissue).
Human esterase D mRNA, 3'end.
49970 LUPUS LA PROTEIN (HUMAN);.
H.sapiens mRNA for TRAP beta subunit.
125446 TRANSCRIPTION INITIATION FACTOR TFIID (Homo sapiens)
Human mRNA for human homologue of rat phosphatidylethanolamine binding protein, complete cds.
120041 HLA-DR ASSOC. PROTEIN I, P31 (also called Ii, In, M1, Dr gamma, XM 1) (Homo sapiens)
Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence.
Homo sapiens integral nuclear envelope inner membrane protein (LBR) gene, complete cds.
52626 HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION (Saccharomyces cerevisiae)
H.sapiens mRNA for ATP-citrate lyase.
Human mRNA for ORF (KIAA0102), complete cds.
238612 Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1 or BSC2) mRNA, complete cds.
26573 STATHMIN (Homo sapiens)
H.sapiens mRNA for DNA primase (subunit p48).
Human c-myb mRNA, 3'end.
Human superoxide dismutase (SOD3 or EC-SOD) gene, complete cds.

FIG. 2E

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Ratio	Repressed EST #	Accession #	EST?	SAGE?
44	47.1	303	0.75	1	6.44	Hsa.1511	V00530 gene 1	☐	☐
45	52.4	299	0.8	0.95	5.7	Hsa.1067	J04543 gene 1	☐	☐
46	50.1	296	0.75	1	5.91	Hsa.1877	M88108 gene 1	☐	☐
47	55.1	294	0.71	0.9	5.33	Hsa.421	D16294 gene 1	☐	☐
48	38.8	290	0.7	0.95	7.48	Hsa.1583	D42084 gene 1	☐	☐
49	-49.3	287	0.62	0.86		Hsa.1625	H59259 3' UTR 1	☑	☐
50	54.3	280	0.76	1	5.16	Hsa.3075	X78627 gene 1	☐	☐
51	43.1	271	0.7	0.95	6.3	Hsa.18494	T93518 3' UTR 2a	☑	☐
52	19.9	264	0.55	0.85	13.3	Hsa.1573	D42041 gene 1	☐	☐
53	46.5	262	0.65	0.94	5.64	Hsa.2490	D21262 gene 1	☐	☐
54	22.1	261	0.67	0.9	11.8	Hsa.1595	L32866 gene 1	☐	☐
55	26.1	253	0.76	0.95	9.67	Hsa.1816	T91855 3' UTR 1	☑	☐
56	10.2	251	0.65	0.8	24.6	Hsa.1490	R56440 3' UTR 1	☑	☐
57	29.9	250	0.65	0.95	8.34	Hsa.9856	R60195 3' UTR 2a	☑	☐
58	10.4	248	0.65	1	23.9	Hsa.150	L10678 gene 1	☑	☐
59	40.2	245	0.95	0.85	6.09	Hsa.7048	R56401 3' UTR 2a	☑	☐
60	6.69	242	0.57	0.95		Hsa.1315	D13639 gene 1	☐	☐
61	41.2	234	0.65	0.95	5.7	Hsa.21993	R12588 3' UTR 2a	☑	☐
62	43.4	234	0.65	0.8	5.38	Hsa.970	M77836 gene 1	☑	☐
63	22.2	211	0.8	0.95	9.51	Hsa.17935	H01943 3' UTR 2a	☑	☐
64	26.6	206	0.57	0.95	7.73	Hsa.10122	T52362 3' UTR 2a	☑	☐
65	27.1	195	0.8	0.85	7.2	Hsa.654	L33930 gene 1	☐	☐

TO FIG. 2F

FIG. 2F

TO FIG. 2E

66	27.2	195	0.7	0.9	7.18	Hsa.10779	X87212 gene 1	☐	☐
67	17	190	0.7	0.95	11.2	Hsa.1815	L31801 gene 1	☐	☐
68	-4.22	189	0.6	0.8		Hsa.3091	T49870 3' UTR 1	☑	☐
69	28.1	187	0.5	0.8	6.65	Hsa.462	U09564 gene 1	☐	☐
70	5.53	186	0.8	0.9		Hsa.42520	H64001 3' UTR 2a	☑	☐
71	21.6	175	0.6	0.8	8.09	Hsa.1460	M20867 gene 1	☐	☐
72	31.8	173	0.6	0.85	5.45	Hsa.14771	T70251 3' UTR 2a	☑	☐
73	20.3	171	0.76	0.86	8.41	Hsa.9868	T50501 3' UTR 2a	☑	☐
74	31.5	169	0.7	1	5.36	Hsa.2892	X76029 gene 1	☐	☐
75	17.7	168	0.67	0.9	9.49	Hsa.1361	M14219 gene 1	☐	☐
76	14.5	166	0.75	1	11.5	Hsa.12976	X74987 gene 1	☐	☐
77	27	164	0.55	0.9	6.06	Hsa.2485	D14694 gene 1	☐	☐
78	-8.48	159	0.37	0.84		Hsa.234	L19183 gene 1	☐	☐
79	30.9	157	0.8	0.9	5.09	Hsa.1242	T55008 3' UTR 1	☑	☐
80	15.8	147	0.7	0.95	9.33	Hsa.25724	R46716 3' UTR 2a	☑	☐
81	28.6	145	0.7	0.85	5.07	Hsa.38007	R88418 3' UTR 2a	☑	☐
82	28.5	145	0.65	0.9	5.09	Hsa.1780	R09502 3' UTR 1	☑	☐
83	23	145	0.7	0.95	6.29	Hsa.1615	D43948 gene 1	☐	☐
84	20.8	142	0.85	0.95	6.82	Hsa.13795	H00297 3' UTR 2a	☑	☐
85	7.23	141	0.55	0.8		Hsa.1665	L23959 gene 1	☐	☐
86	24.6	140	0.67	1	5.67	Hsa.928	M22538 gene 1	☑	☐

FIG. 2G

Gene Description — Repressed
Human mRNA encoding IMP:pyrophosphate phosphoribosyltransferase E.C. 2.4.2.8.
Human synexin mRNA, complete cds.
Human p62 mRNA, complete cds.
Human mRNA for mitochondrial 3-oxoacyl-CoA thiolase, complete cds.
Human mRNA (KIAA0094) for ORF (yeast methionine aminopeptidase-related), partial cds.
204299 REPLICATION PROTEIN A 14 KD SUBUNIT (HUMAN);.
H.sapiens mRNA for translin.
117708 MYOSIN HEAVY CHAIN, CLONE 203 (Hydra attenuata)
Human mRNA (KIAA0088) for ORF (alpha-glucosidase-related), partial cds.
Human mRNA (KIAA0035) for ORF (rat 140kd nucleolar phosphoprotein homologue), partial cds.
Human effector cell protease receptor-1 (EPR-1) gene, partial cds.
112020 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (HUMAN);.
40874 TUBULIN GAMMA CHAIN (HUMAN);.
42829 EUKARYOTIC INITIATION FACTOR 4B (Homo sapiens)
PROFILIN II (HUMAN);.
40753 RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN, RanGAP (Homo sapiens)
Human mRNA for ORF (KIAK0002), or HUMAN D-TYPE CYCLIN complete cds.
128385 HAMSTER RNA FOR CYCLIN B2 (mesocricetus auratus)
PYRROLINE-5-CARBOXYLATE REDUCTASE (HUMAN);.
150169 EUKARYOTIC INITIATION FACTOR 4E (Homo sapiens)
72050 NUCLEOTIDE-SENSITIVE CHLORIDE CHANNEL (Canis familiaris), or HUMAN CHLORIDE CHANNEL REGULATORY PROTEIN mRNA

TO FIG. 2H

FIG. 2H

TO FIG. 2G

Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region.
H.sapiens mRNA for cathepsin C (dipeptidyl peptidase I).
Homo sapiens monocarboxylate transporter 1 (SLC16A1) mRNA, complete cds.
68690 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (HUMAN).
Human serine kinase (SRPK1) mRNA, complete cds.
209484 CD9 ANTIGEN (Bos taurus), or HUMAN T245 PROTEIN
Human glutamate dehydrogenase (GDH) mRNA, complete cds.
109334 NEGATIVE REGULATOR OF MITOSIS (Emericella nidulans)
77138 EUKARYOTIC INITIATION FACTOR 1A (Sac cerevisiae), or HUMAN PROTEIN SYNTHESIS FACTOR 4C(eIF-4C)
H.sapiens mRNA for neuromedin U.
Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.
H.sapiens mRNA for 2'-5' oligoadenylate binding protein.
Human mRNA (KIAA0024) for ORF (putative human counterpart of chinese hamster phosphatidylserine synthase gene), complete cds.
Human MAC30 mRNA, 3' end.
74167 APOLIPOPROTEIN A-II PRECURSOR (HUMAN).
36504 GTPASE ACTIVATING PROTEIN ROTUND (Drosophila melanogaster)
166353 CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (Homo sapiens)
127707 LAMININ BETA-1 CHAIN PRECURSOR (HUMAN);.
Human mRNA (KIAA0097) for ORF (novel protein), complete cds.
149556 O-ANTIGEN POLYMERASE (Shigella flexneri)
Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds.
NADH-UBIQUINONE DEHYDROGENASE 24 KD SUBUNIT PRECURSOR (HUMAN);.

FIG. 2I

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Repressed Ratio	EST #	Accession #	EST?	SAGE?
87	27.1	139	0.8	0.9	5.14	Hsa.1811	M37510 gene 1	☐	☐
88	17.2	137	0.4	0.9	7.95	Hsa.6633	R61359 3' UTR 2a	☑	☐
89	20.8	136	0.4	0.9	6.55	Hsa.13172	T73788 3' UTR 2a	☑	☐
90	19.7	135	0.65	0.85	6.85	Hsa.1423	J04102 gene 1	☐	☐
91	18.1	134	0.57	0.9	7.41	Hsa.13967	T66747 3' UTR 2a	☑	☐
92	19.2	134	0.7	1	6.96	Hsa.1245	M21154 gene 1	☑	☐
93	7.16	132	0.71	1		Hsa.13508	R37660 3' UTR 2a	☑	☐
94	-0.0563	130	0.65	0.85		Hsa.28663	H10045 3' UTR 2a	☑	☐
95	6.27	129	0.55	0.95		Hsa.1200	D38553 gene 1	☐	☐
96	8.89	128	0.67	0.9		Hsa.2070	J04088 gene 1	☐	☐
97	1.42	124	0.7	0.9		Hsa.45678	H88978 3' UTR 2a	☐	☐
98	13.2	123	0.45	0.9	9.27	Hsa.18077	H02009 3' UTR 2a	☑	☐
99	12.3	121	0.62	0.95	9.84	Hsa.1219	M16827 gene 1	☐	☐
100	10.9	119	0.5	0.9	11	Hsa.1952	T96666 3' UTR 1	☑	☐

FIG. 2J

Repressed Gene Description
Human methylmalonyl CoA mutase (MUT) gene, exon 13.
37866 BASIGIN PRECURSOR (Gallus gallus)
84443 GA BINDING PROTEIN BETA-1 CHAIN (Homo sapiens)
Human erythroblastosis virus oncogene homolog 2 (ets-2) mRNA, complete cds.
53193 26S PROTEASE REGULATORY SUBUNIT 6 (Homo sapiens)
S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (HUMAN);.
26573 STATHMIN (Homo sapiens)
46827 VAV ONCOGENE (Homo sapiens)
Human mRNA (KIAA0074) for ORF (yeast C728 protein-related), partial cds.
Human DNA topoisomerase II gene (top2), gene 1
Homo sapiens cDNA clone 253186 3'
151010 EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (Homo sapiens)
Human medium-chain acyl-CoA dehydrogenase (ACADM) mRNA, complete cds.
121357 A49436 CDI1=CYCLIN-DEPENDENT KINASE INTERACTOR 1 - ;.

INTERNATIONAL SEARCH REPORT

Inter ›nal Application No
PCT/US 99/06656

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	EP 0 390 323 A (UNIV JOHNS HOPKINS) 3 October 1990 (1990-10-03) the whole document ---	1-30, 46-66
Y	SCHENA M ET AL: "PARALLEL HUMAN GENOME ANALYSIS: MICROARRAY-BASED EXPRESSION MONITORING OF 1000 GENES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 93, no. 20, 1 October 1996 (1996-10-01), pages 10614-10619, XP002912238 ISSN: 0027-8424 the whole document ---	1-30, 46-66
Y	WO 95 19369 A (UNIV VANDERBILT) 20 July 1995 (1995-07-20) see whole doc. esp.claims --- -/--	1-66

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
9 July 1999	16/07/1999

Name and mailing address of the ISA	Authorized officer
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INTERNATIONAL SEARCH REPORT

Inter. ...nal Application No
PCT/US 99/06656

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages.	Relevant to claim No.
Y	MADDEN S ET AL: "SAGE transcription profiles for P53-dependent growth regulation" ONCOGENE, vol. 15, no. 9, 1 August 1997 (1997-08-01), pages 1079-1085, XP002083784 ISSN: 0950-9232 see whole doc. esp. abstract and discussion	1-66
Y	WO 94 18992 A (ONYX PHARMACEUTICALS) 1 September 1994 (1994-09-01) see whole doc, esp. claims	42,43
Y	MADDEN S L ET AL: "INDUCTION OF CELL GROWTH REGULATORY GENES BY P53" CANCER RESEARCH, vol. 56, no. 23, 1 December 1996 (1996-12-01), pages 5384-5390, XP002046025 ISSN: 0008-5472 the whole document	42,43
A	BEAUDRY G ET AL: "Therapeutic targeting of the P53 tumor suppressor gene" CURRENT OPINION IN BIOTECHNOLOGY, vol. 7, no. 7, 1 December 1996 (1996-12-01), pages 592-600, XP002083786 ISSN: 0958-1669 see whole doc, esp. p.593,2.col, table 2 and 3	
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